1812
#10
MB
07/28/97

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/462,355A

CRF Processing Date: 7/12/97
Edited by: _____
Verified by: _____ (STIC staff)

- [x] Changed a file from non-ASCII to ASCII
- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- [ ] Edited a format error in the Current Application Data section, specifically: ENTERED _____
- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- [ ] Added the mandatory heading and subheadings for "Current Application Data".
- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- [ ] Inserted colons after headings/subheadings. Headings edited included: _____
- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____
- [ ] Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- [ ] Inserted mandatory headings, specifically: _____
- [ ] Corrected an obvious error in the response, specifically: _____
- [x] Edited identifiers where upper case is used but lower case is required, or vice versa. Seq 1
- [ ] Corrected an error in the Number of Sequences field, specifically: _____
- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- [ ] Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- [ ] Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

SEQUENCE LISTING

(1) General Information

(i) APPLICANT: Coleman, Roger
Au-Young, Janice
Bandman, Olga
Seilhamer, Jeffrey J.

(ii) TITLE OF THE INVENTION: A C5a-LIKE SEVEN TRANSMEMBRANE RECEPTOR

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/462,355
(B) FILING DATE: June 5, 1995

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy .
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0040 US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: Mast Cell
(B) CLONE: 8118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGTCTT TCTCTGCTGA GACCAATTCA ACTGACCTAC TCTCACAGCC ATGGAATGAG 60

CCCCCAGTAA TTCTCTCCAT GGTCATTCTC AGCCTTACTT TTTTACTGGG ATTGCCAGGC 120

AATGGGCTGG TGCTGTGGGT GGCTGGCCTG AAGATGCAGC GGACAGTGAA CACAATTTGG 180

TTCCTCCACC TCACCTTGGC GGACCTCCTC TGCTGCCTCT CCTTGGCCTT CTCGCTGGCT 240

CACTTGGCTC TCCAGGGACA GTGGCCCTAC GGCAGGTTCC TATGCAAGCT CATCCCCTCC 300

ATCATTGTCC TCAACATGTT TGGCAGTGTC TTCCTGCTTA CTGCCATTAG CCTGGATCGC 360

TGTCTTGTGG TATTCAAGCC AATCTGGTGT CAGAATCATC GCAATGTAGG GATGGCCTGC 420

TCTATCTGTG GATGTATCTG GGTGGTGGCT TTTGTGTTGT GCATTCCTGT GTTCGTGTAC 480

CGGGAAATCT TCACTACAGA CAACCATAAT AGATGTGGCT ACAAATTTGG TCTCTCCAGC 540

TCATTAGATT ATCCAGACTT TTATGGGGAT CCACTAGAAA ACAGGTCTCT TGAAAACATT 600

GTTCAGCCGC CTGGAGAAAT GAATGATAGG TTAGATCCTT CCTCTTTCCA AACAAATGAT 660

CATCCTTGGA CAGTCCCCAC TGTCTTCCAA CCTCAAACAT TTCAAAGACC TTCTGCAGAT 720

TCACTCCCTA GGGGTTCTGC TAGGTTAACA AGTCAAAATC TGTATTCTAA TGTATTTAAA 780

CCTGCTGATG TGGTCTCACC TAAAATCCCC AGTGGGTTTC CTATTGAAGA TCACGAAACC 840

AGCCCACTGG ATAACTCTGA TGCTTTTCTC TCTACTCATT TAAAGCTGTT CCCTAGCGCT 900

TCTAGCAATT CCTTCTACGA GTCTGAGCTA CCACAAGGTT TCCAGGATTA TTACAATTTA 960

GGCCAATTCA CAGATGACGA TCAAGTGCCA ACACCCCTCG TGGCAATAAC GATCACTAGG 1020

CTAGTGGTGG GTTTCCTGCT GCCCTCTGTT ATCATGATAG CCTGTTACAG CTTCATTGTC 1080

TTCCGAATGC AAAGGGGCCG CTTCGCCAAG TCTCAGAGCA AAACCTTTCG AGTGGCCGTG 1140

GTGGTGGTGG CTGTCTTTCT TGTCTGCTGG ACTCCATACC ACATTTGGGG AGTCCTGTCA 1200

TTGCTTACTG ACCCAGAAAC TCCCTTGGGG AAAACTCTGA TGTCCTGGGA TCATGTATGC 1260

ATTGCTCTAG CATCTGCCAA TAGTTGCTTT AATCCCTTCC TTTATGCCCT CTTGGGGAAA 1320

GATTTTAGGA AGAAAGCAAG GCAGTCCATT CAGGGAATTC TGGAGGCAGC CTTCAGTGAG 1380

GAGCTCACAC GTTCCACCCA CTGTCCCTCA AACAATGTCA TTTCAGAAAG AAATAGTACA 1440

ACTGTG 1446

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Ala Ser Phe Ser Ala Glu Thr Asn Ser Thr Asp Leu Leu Ser Gln
 1               5                  10                  15

Pro Trp Asn Glu Pro Pro Val Ile Leu Ser Met Val Ile Leu Ser Leu
            20                  25                  30

Thr Phe Leu Leu Gly Leu Pro Gly Asn Gly Leu Val Leu Trp Val Ala
        35                  40                  45

Gly Leu Lys Met Gln Arg Thr Val Asn Thr Ile Trp Phe Leu His Leu
    50                  55                  60

Thr Leu Ala Asp Leu Leu Cys Cys Leu Ser Leu Ala Phe Ser Leu Ala
65                  70                  75                  80

His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys
                85                  90                  95

Leu Ile Pro Ser Ile Ile Val Leu Asn Met Phe Gly Ser Val Phe Leu
            100                 105                 110

Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Val Val Phe Lys Pro Ile
        115                 120                 125

Trp Cys Gln Asn His Arg Asn Val Gly Met Ala Cys Ser Ile Cys Gly
```

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153      130                 135                 140
154
155  Cys Ile Trp Val Val Ala Phe Val Leu Cys Ile Pro Val Phe Val Tyr
156  145                 150                 155                 160
157
158  Arg Glu Ile Phe Thr Thr Asp Asn His Asn Arg Cys Gly Tyr Lys Phe
159                  165                 170                 175
160
161  Gly Leu Ser Ser Ser Leu Asp Tyr Pro Asp Phe Tyr Gly Asp Pro Leu
162              180                 185                 190
163
164  Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn
165          195                 200                 205
166
167  Asp Arg Leu Asp Pro Ser Ser Phe Gln Thr Asn Asp His Pro Trp Thr
168      210                 215                 220
169
170  Val Pro Thr Val Phe Gln Pro Gln Thr Phe Gln Arg Pro Ser Ala Asp
171  225                 230                 235                 240
172
173  Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser
174                  245                 250                 255
175
176  Asn Val Phe Lys Pro Ala Asp Val Val Ser Pro Lys Ile Pro Ser Gly
177              260                 265                 270
178
179  Phe Pro Ile Glu Asp His Glu Thr Ser Pro Leu Asp Asn Ser Asp Ala
180          275                 280                 285
181
182  Phe Leu Ser Thr His Leu Lys Leu Phe Pro Ser Ala Ser Ser Asn Ser
183      290                 295                 300
184
185  Phe Tyr Glu Ser Glu Leu Pro Gln Gly Phe Gln Asp Tyr Tyr Asn Leu
186  305                 310                 315                 320
187
188  Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile
189                  325                 330                 335
190
191  Thr Ile Thr Arg Leu Val Val Gly Phe Leu Leu Pro Ser Val Ile Met
192              340                 345                 350
193
194  Ile Ala Cys Tyr Ser Phe Ile Val Phe Arg Met Gln Arg Gly Arg Phe
195          355                 360                 365
196
197  Ala Lys Ser Gln Ser Lys Thr Phe Arg Val Ala Val Val Val Val Ala
198      370                 375                 380
199
200  Val Phe Leu Val Cys Trp Thr Pro Tyr His Ile Trp Gly Val Leu Ser
201  385                 390                 395                 400
202
203  Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp
204                  405                 410                 415
205
```

```
Asp His Val Cys Ile Ala Leu Ala Ser Ala Asn Ser Cys Phe Asn Pro
            420                 425                 430

Phe Leu Tyr Ala Leu Leu Gly Lys Asp Phe Arg Lys Lys Ala Arg Gln
        435                 440                 445

Ser Ile Gln Gly Ile Leu Glu Ala Ala Phe Ser Glu Glu Leu Thr Arg
    450                 455                 460

Ser Thr His Cys Pro Ser Asn Asn Val Ile Ser Glu Arg Asn Ser Thr
465                 470                 475                 480

Thr Val
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAAGACAGC CACCACCACC ACG 23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGAAAGCAAG GCAGTCCATT CAGG 24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Asn Ser Phe Asn Tyr Thr Thr Pro Asp Tyr Gly His Tyr Asp Asp
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/462,355A*

INPUT SET: S19020.raw

Line	Error	Original Text

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

ASCII conversion

```
                                SEQUENCE LISTING

(1)    General Information

        (i) APPLICANT: Coleman, Roger
                       Au-Young, Janice
                       Bandman, Olga
                       Seilhamer, Jeffrey J.

        (ii) TITLE OF THE INVENTION: A C5a-LIKE SEVEN TRANSMEMBRANE RECEPTOR

--> 01  (iii) NUMBER OF SEQUENCES: 5

        (iv) CORRESPONDENCE ADDRESS:
          (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
          (B) STREET: 3174 Porter Drive
          (C) CITY: Palo Alto
          (D) STATE: CA
          (E) COUNTRY: USA
          (F) ZIP: 94304

        (v) COMPUTER READABLE FORM:
          (A) MEDIUM TYPE: Diskette
          (B) COMPUTER: IBM Compatible
          (C) OPERATING SYSTEM: DOS
          (D) SOFTWARE: FastSEQ for Windows Version 2.0

        (vi) CURRENT APPLICATION DATA:
          (A) APPLICATION NUMBER: 08/462,355
          (B) FILING DATE: June 5, 1995

        (vii) PRIOR APPLICATION DATA:
          (A) APPLICATION NUMBER:
          (B) FILING DATE:

        (viii) ATTORNEY/AGENT INFORMATION:
          (A) NAME: Billings, Lucy .
          (B) REGISTRATION NUMBER: 36,749
          (C) REFERENCE/DOCKET NUMBER: PF-0040 US

        (ix) TELECOMMUNICATION INFORMATION:
          (A) TELEPHONE: 415-855-0555
          (B) TELEFAX: 415-845-4166
```

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO:1:

(i) (I) **SEQUENCE CHARACTERISTICS:**
(A) LENGTH: 1446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: Mast Cell
(B) CLONE: 8118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGTCTT TCTCTGCTGA GACCAATTCA ACTGACCTAC TCTCACAGCC ATGGAATGAG 60

CCCCCAGTAA TTCTCTCCAT GGTCATTCTC AGCCTTACTT TTTTACTGGG ATTGCCAGGC 120

AATGGGCTGG TGCTGTGGGT GGCTGGCCTG AAGATGCAGC GGACAGTGAA CACAATTTGG 180

TTCCTCCACC TCACCTTGGC GGACCTCCTC TGCTGCCTCT CCTTGGCCTT CTCGCTGGCT 240

CACTTGGCTC TCCAGGGACA GTGGCCCTAC GGCAGGTTCC TATGCAAGCT CATCCCCTCC 300

ATCATTGTCC TCAACATGTT TGGCAGTGTC TTCCTGCTTA CTGCCATTAG CCTGGATCGC 360

TGTCTTGTGG TATTCAAGCC AATCTGGTGT CAGAATCATC GCAATGTAGG GATGGCCTGC 420

TCTATCTGTG GATGTATCTG GGTGGTGGCT TTTGTGTTGT GCATTCCTGT GTTCGTGTAC 480

CGGGAAATCT TCACTACAGA CAACCATAAT AGATGTGGCT ACAAATTTGG TCTCTCCAGC 540

TCATTAGATT ATCCAGACTT TTATGGGGAT CCACTAGAAA ACAGGTCTCT TGAAAACATT 600

GTTCAGCCGC CTGGAGAAAT GAATGATAGG TTAGATCCTT CCTCTTTCCA AACAAATGAT 660

CATCCTTGGA CAGTCCCCAC TGTCTTCCAA CCTCAAACAT TTCAAAGACC TTCTGCAGAT 720

TCACTCCCTA GGGGTTCTGC TAGGTTAACA AGTCAAAATC TGTATTCTAA TGTATTTAAA 780

CCTGCTGATG TGGTCTCACC TAAAATCCCC AGTGGGTTTC CTATTGAAGA TCACGAAACC 840

AGCCCACTGG ATAACTCTGA TGCTTTTCTC TCTACTCATT TAAAGCTGTT CCCTAGCGCT 900

TCTAGCAATT CCTTCTACGA GTCTGAGCTA CCACAAGGTT TCCAGGATTA TTACAATTTA 960

GGCCAATTCA CAGATGACGA TCAAGTGCCA ACACCCCTCG TGGCAATAAC GATCACTAGG 1020